

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 7, 2005, 07:04:17 ; Search time 20.4798 Seconds

(without alignments)  
1193.323 Million cell updates/sec

Title: US-09-939-537-33

Perfect score: 1385

Sequence: 1 BKSCDKHTHCPCPCAPBL.....DETCARAGQDGLDGLWTTDP 254

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1258	90.8	330	1 GHNU	Ig gamma-1 chain C
2	1252	90.4	374	2 S69339	Ig heavy chain V r
3	1250	90.3	255	4 S31866	Ig gamma-1 chain C
4	1210	87.4	234	2 PT0207	Ig gamma chain C r
5	1171	84.5	377	2 A23511	Ig gamma-3 chain C
6	1169	84.4	377	2 A60764	Ig gamma-3 chain C
7	1151	83.1	289	1 G3HWT	Ig gamma-3 heavy C
8	1140	82.3	326	1 G2HU	Ig gamma-2 chain C
9	1130	81.6	327	1 G4HU	Ig gamma-4 chain C
10	938.5	67.8	398	1 G3MSM	Ig gamma-3 chain C
11	931.5	67.3	393	1 G3MSM	Ig gamma-1 chain C
12	916	66.1	323	1 GHBP	Ig gamma chain C r
13	905	65.3	399	1 G2MSAM	Ig gamma-2a chain
14	901.5	65.1	328	2 I47160	Ig gamma 2b chain
15	901.5	65.1	328	2 I47159	Ig gamma 2a chain
16	898	64.8	277	2 I47162	Ig gamma 4 chain C
17	896	64.7	329	1 G2GP	Ig gamma-2 chain C
18	880.5	63.6	328	2 I47158	Ig gamma 1 chain C
19	873.5	63.1	328	2 I47161	Ig gamma 3 chain C
20	870.5	62.9	405	1 G2MSBM	Ig gamma-2b chain
21	851	61.4	470	2 S22080	Ig heavy chain pre
22	842.5	60.8	308	2 C30554	Ig heavy chain C r
23	842.5	60.8	472	2 S31459	Ig gamma-1 chain -
24	840.5	60.7	329	1 G3MSC	Ig gamma-3 chain C
25	837	60.4	333	2 PS0018	Ig gamma-2b chain
26	827.5	59.7	444	2 PC4436	monoclonal antibod
27	817.5	59.0	324	1 G1MS	Ig gamma-1 chain C
28	817.5	59.0	326	2 PS0017	Ig gamma-1 chain C
29	804.5	58.1	329	2 S00847	Ig gamma-2c chain

30	804	58.1	330	1 G2MSA	Ig gamma-2a chain
31	804	58.1	469	2 S37483	Ig gamma-2a chain
32	800	57.8	335	1 G2MSAB	Ig gamma-2a chain
33	794	57.3	446	2 S40295	Ig gamma-2a chain
34	780.5	56.4	322	2 PS0019	Ig gamma-2a chain
35	774.5	55.9	474	1 G2MS11	Ig gamma-2b chain
36	759	54.8	327	2 S06611	Ig gamma-2 chain C
37	754.5	54.5	475	2 S01321	Ig gamma-2b chain
38	702	50.7	180	2 I46732	Ig gamma heavy cha
39	574.5	41.5	218	2 A36040	Ig heavy chain V-I
40	572.5	41.3	249	2 S69340	Ig heavy chain VHI
41	566	40.9	152	2 S14236	Ig gamma-1 chain C
42	390.5	28.2	572	2 B46529	Ig y heavy chain (
43	363.5	26.2	476	1 MHMSM	Ig mu chain C regi
44	359	25.9	549	2 S04845	Ig heavy chain pre
45	357.5	25.8	627	2 S14683	Ig mu chain precu

#### ALIGNMENTS

##### RESULT 1

GHNU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C>Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004

C/Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R/Elison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A>Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A/Reference number: A93433; MUID:82274238; PMID:6287432

A/Accession: A93433

A/Molecule type: DNA

A/Residues: 1-330 <ELL>

A/Cross-references: UNIPROT:P01857; EMBL:Z17370

A/Note: this sequence has the Gln(17) allotypic marker, 97-Lys, and the Gln(1) markers, ;

A/Note: Lys-330 is removed after translation

R/Harris, L.J.

submitted to the EMBL Data Library, October 1992

A/Reference number: S33904

A/Accession: S36861

A/Molecule type: DNA

A/Residues: 2-330 <HAR>

A/Cross-references: EMBL:Z17370

R/Rakhaishi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A>Title: Structure of human immunoglobulin gamma genes: implications for evolution of a ;

A/Reference number: S33887; MUID:83001943; PMID:681139

A/Accession: S33887

A/Molecule type: DNA

A/Residues: 88-113/235-330 <TRK>

A/Cross-references: EMBL:Z17370

R/Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.U.; Edelman, C

Biochemistry 9, 3161-3170, 1970

A>Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen

A/Reference number: A90564; MUID:71064024; PMID:5489771

A/Contents: myeloma protein Bu

A/Accession: B90563

A/Molecule type: protein

A/Residues: 1-96, 'R', 98-135 <GUN>

A/Note: this sequence has the Gln(3) marker, 97-Arg

R/Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A>Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequer

A/Reference number: A90564; MUID:71064025; PMID:5530842

A/Contents: Bu

A/Accession: A90564

A/Molecule type: protein

A/Residues: 156-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240, 'R';

Hope-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A>Title: Die Primarstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein N1e),

Igen Primaerstruktur.

A:Reference number: A91668; MUID:77070269; PMID:826475

A:Contents: myeloma protein Nie

A:Accession: B91668

A:Molecule type: protein

A:Residues: 1-34, 'Q', '36-96', 'K', '98-115', 'Q', '117-197', 'D', '199-238', 'D', '240', 'L', '242-268', 'E', '27

A:Note: this sequence has the G1m(17) and G1m(1) markers

R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.

Hope-Seyler's Z. Physiol. Chem. 364, 713-727, 1969

A:Title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL

A:Reference number: A91723; MUID:83289131; PMID:6884994

A:Contents: myeloma protein KOL; disulfide bonds

A:Accession: A91723

A:Molecule type: protein

A:Residues: 1-96, 'R', '98-197', 'D', '199-238', 'E', '240', 'W', '242-266', 'D', '268-271', 'D', '273-330' <SCH

A:Note: this sequence has the G1m(3) and G1m(non-1) markers

R:Gall, W.E.; Edelman, G.M.

Biochemistry 9, 3188-3196, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid

A:Reference number: A90565; MUID:71064027; PMID:4923144

A:Contents: annotation; disulfide bonds

R:Decker, U.; Schwarz, J.; Reichel, W.; Hilschmann, N.

Hope-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976

A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob

A:Reference number: A91667; MUID:77070267; PMID:1002129

A:Contents: annotation; disulfide bonds

C:Genetics:

A:Gene: GDB:IGHG1

A:Cross-references: GDB:120085; OMIM:147100

A:Map position: 14q32.33-14q32.33

A:Introns: 99/1; 114/1; 224/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:20-85/Domain: immunoglobulin homology <IM1>

F:137-206/Domain: immunoglobulin homology <IM2>

F:243-310/Domain: immunoglobulin homology <IM3>

F:27-83, 144-204, 250-308/Disulfide bonds: #status experimental

F:103/Disulfide bonds: interchain (to light chain) #status experimental

F:109, 112/Disulfide bonds: interchain (to heavy chain) #status experimental

F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 90.8%; Score 1258; DB 1; Length 330;

Best Local Similarity 100.0%; Pred. No. 4, 1e-88;

Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 60

Db 99 EPKSCDKHTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 158

QY 61 NMVYDGEVHNAKTRPREQYNSTYRVSVLT/HLHOMLNKGEYKCKVSKALPAPIEKT 120

Db 159 NMVYDGEVHNAKTRPREQYNSTYRVSVLT/HLHOMLNKGEYKCKVSKALPAPIEKT 218

QY 121 ISKAGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEMESNGQPENNYKTTTP 180

Db 219 ISKAGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEMESNGQPENNYKTTTP 278

QY 181 PVLDSGSGFFLYSKLTVDKSRMNOGQNFVSCVMHDLNHTYQKSLISLSPG 231

Db 279 PVLDSGSGFFLYSKLTVDKSRMNOGQNFVSCVMHDLNHTYQKSLISLSPG 329

RESULT 2

S69339

Ig heavy chain V region precursor - human

C:Species: Homo sapiens (man)

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000

C:Accession: S69339; S72664

R:Thamlich, A.A.; Aucuttier, P.; Preud'homme, J.L.; Cogne, M.

Eur. J. Biochem. 229, 54-60, 1995

A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.

A:Reference number: S69339; MUID:95262687; PMID:7744049

A:Accession: S69339

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-374 <KHA>

A:Cross-references: EMBL:X81695

R:Thamlich, A.A.

Submitted to the EMBL Data Library, September 1994

A:Reference number: S72664

A:Accession: S72664

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-140, 'C', '142-374' <KHA>

A:Cross-references: EMBL:X81695

C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 90.4%; Score 1252; DB 2; Length 374;

Best Local Similarity 99.1%; Pred. No. 1, 4e-87;

Matches 229; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 60

Db 143 EPKSCDKHTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 202

QY 61 NMVYDGEVHNAKTRPREQYNSTYRVSVLT/HLHOMLNKGEYKCKVSKALPAPIEKT 120

Db 203 NMVYDGEVHNAKTRPREQYNSTYRVSVLT/HLHOMLNKGEYKCKVSKALPAPIEKT 262

QY 121 ISKAGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEMESNGQPENNYKTTTP 180

Db 263 ISKAGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEMESNGQPENNYKTTTP 322

QY 181 PVLDSGSGFFLYSKLTVDKSRMNOGQNFVSCVMHDLNHTYQKSLISLSPG 231

Db 323 PVLDSGSGFFLYSKLTVDKSRMNOGQNFVSCVMHDLNHTYQKSLISLSPG 373

RESULT 3

S31866

Ig gamma-1 chain C region - synthetic

C:Species: synthetic

A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli;

C>Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000

C:Accession: S31866

R:Filipula, D.

Submitted to the EMBL Data Library, February 1993

A:Description: Screening method for protein-protein interactions of cloned gene products.

A:Reference number: S31866

A:Accession: S31866

A:Molecule type: mRNA

A:Residues: 1-255 <FIL>

A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069

F:1-32/Region: Escherichia coli outer membrane protein A precursor

F:23-25/Region: human Ig gamma-1 chain C region

Query Match 90.3%; Score 1250; DB 4; Length 255;

Best Local Similarity 99.6%; Pred. No. 1, 2e-87;

Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 60

Db 24 EPKSCDKHTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 83

QY 61 NMVYDGEVHNAKTRPREQYNSTYRVSVLT/HLHOMLNKGEYKCKVSKALPAPIEKT 120

Db 84 NMVYDGEVHNAKTRPREQYNSTYRVSVLT/HLHOMLNKGEYKCKVSKALPAPIEKT 143

QY 121 ISKAGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEMESNGQPENNYKTTTP 180

Db 144 ISKAGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEMESNGQPENNYKTTTP 203

QY 181 PVLSDSGSFFLYSKLTVDKSRMOQGNVFCSCVHMBALHNHYTKSLSLSPG 231  
 Db 204 PVLSDSGSFFLYSKLTVDKSRMOQGNVFCSCVHMBALHNHYTKSLSLSPG 254

## RESULT 4

PT0207  
 Ig gamma chain C region - chimpanzee  
 C/Species: Pan troglodytes (chimpanzee)  
 C/Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 16-Jul-1999  
 C/Accession: PT0207  
 R/Shrlich, P.H.; Moustafa, Z.A.; Oestberg, L.  
 M.O. Immunol. 28, 319-322, 1991  
 A/Title: Nucleotide sequence of chimpanzee Ig C and hinge regions.  
 A/Reference number: PT0207; PMID:91287716; PMID:2062315  
 A/Accession: PT0207  
 A/Molecule type: mRNA  
 A/Residues: 1-234 <EHR>  
 C/Superfamily: immunoglobulin C region; immunoglobulin homology  
 C/Keywords: immunoglobulin  
 F/48-117/Domain: immunoglobulin homology <IMM>

Query Match 87.4%; Score 1210; DB 2; Length 234;  
 Best Local Similarity 98.7%; Pred. No. 1.2e-84;  
 Matches 222; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EPKSCDTHTCPCPAPABELLIGSPSVLFPKPKDTHMISTPPTVCVVDVSHEDPEVKF 60  
 Db 10 EPKSCDTHTCPCPAPABELLIGSPSVLFPKPKDTHMISTPPTVCVVDVSHEDPEVKF 69  
 QY 61 NMVVDGVEVHNAKTKREBQYNSTYRVSVLTVLHODMLNGKEYKCKVSNKALPAPIEKT 120  
 Db 70 NMVVDGVEVHNAKTKREBQYNSTYRVSVLTVLHODMLNGKEYKCKVSNKALPAPIEKT 129  
 QY 121 ISKAKQPREPQYTYLPPSRDELTKQVSLTCLVKGFYPSDIAVEMESNQPENNYKTTT 180  
 Db 130 ISKAKQPREPQYTYLPPSRDELTKQVSLTCLVKGFYPSDIAVEMESNQPENNYKTTT 189  
 QY 181 PVLSDSGSFFLYSKLTVDKSRMOQGNVFCSCVHMBALHNHYTKS 225  
 Db 190 PVLSDSGSFFLYSKLTVDKSRMOQGNVFCSCVHMBALHNHYTKS 234

## RESULT 5

A23511  
 Ig gamma-3 chain C region (allotype G3m(b)) - human  
 C/Species: Homo sapiens (man)  
 C/Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999  
 C/Accession: A23511  
 R.Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.  
 Nucleic Acids Res. 14, 1779-1789, 1986  
 A/Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: cDNA  
 A/Reference number: A23511; PMID:86148507; PMID:3081877  
 A/Accession: A23511  
 A/Molecule type: DNA  
 A/Residues: 1-377 <HUC>  
 A/Cross-references: GB:X03604; GB:M12958; NID:933070; PIDD:CAA27268.1; PID:9577056  
 C/Genetics:  
 A/Genes: GDB:IGHG3  
 A/Cross-references: GDB:119339; OMIM:147120  
 A/Map position: 14q32.3-14q32.33  
 A/Features: 96/3; 115/3; 130/3; 145/3; 160/3; 270/3  
 C/Superfamily: immunoglobulin C region; immunoglobulin homology  
 C/Keywords: immunoglobulin  
 F/20-85/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 1171; DB 2; Length 377;  
 Best Local Similarity 92.6%; Pred. No. 1.9e-81;  
 Matches 214; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 EPKSCDTHTCPCPAPABELLIGSPSVLFPKPKDTHMISTPPTVCVVDVSHEDPEVKF 60  
 Db 146 EPKSCDTHTCPCPAPABELLIGSPSVLFPKPKDTHMISTPPTVCVVDVSHEDPEVKF 205

QY 61 NMVVDGVEVHNAKTKREBQYNSTYRVSVLTVLHODMLNGKEYKCKVSNKALPAPIEKT 120  
 Db 206 NMVVDGVEVHNAKTKREBQYNSTYRVSVLTVLHODMLNGKEYKCKVSNKALPAPIEKT 265

QY 121 ISKAKQPREPQYTYLPPSRDELTKQVSLTCLVKGFYPSDIAVEMESNQPENNYKTTT 180  
 Db 266 ISKAKQPREPQYTYLPPSRDELTKQVSLTCLVKGFYPSDIAVEMESNQPENNYKTTT 325

QY 181 PVLSDSGSFFLYSKLTVDKSRMOQGNVFCSCVHMBALHNHYTKSLSLSPG 231  
 Db 326 PVLSDSGSFFLYSKLTVDKSRMOQGNVFCSCVHMBALHNHYTKSLSLSPG 376

## RESULT 6

A60764  
 Ig gamma-3 chain C region, form IAT - human  
 C/Species: Homo sapiens (man)  
 C/Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 09-Jul-2004  
 C/Accession: A60764  
 R.Huck, S.; Lefranc, G.; Lefranc, M.P.  
 Immunogenetics 30, 250-257, 1989  
 A/Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert  
 A/Reference number: A60764; PMID:9007613; PMID:2571587  
 A/Accession: A60764  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-377 <HUC>  
 A/Cross-references: UNIPROT:Q8N4Y9  
 C/Superfamily: immunoglobulin C region; immunoglobulin homology  
 C/Keywords: immunoglobulin  
 F/20-85/Domain: immunoglobulin homology <IMM>

Query Match 84.4%; Score 1169; DB 2; Length 377;  
 Best Local Similarity 92.6%; Pred. No. 2.7e-81;  
 Matches 214; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 EPKSCDTHTCPCPAPABELLIGSPSVLFPKPKDTHMISTPPTVCVVDVSHEDPEVKF 60  
 Db 146 EPKSCDTHTCPCPAPABELLIGSPSVLFPKPKDTHMISTPPTVCVVDVSHEDPEVKF 205  
 QY 61 NMVVDGVEVHNAKTKREBQYNSTYRVSVLTVLHODMLNGKEYKCKVSNKALPAPIEKT 120  
 Db 206 NMVVDGVEVHNAKTKREBQYNSTYRVSVLTVLHODMLNGKEYKCKVSNKALPAPIEKT 265  
 QY 121 ISKAKQPREPQYTYLPPSRDELTKQVSLTCLVKGFYPSDIAVEMESNQPENNYKTTT 180  
 Db 266 ISKAKQPREPQYTYLPPSRDELTKQVSLTCLVKGFYPSDIAVEMESNQPENNYKTTT 325  
 QY 181 PVLSDSGSFFLYSKLTVDKSRMOQGNVFCSCVHMBALHNHYTKSLSLSPG 231  
 Db 326 PVLSDSGSFFLYSKLTVDKSRMOQGNVFCSCVHMBALHNHYTKSLSLSPG 376

## RESULT 7

G3HWM1  
 Ig gamma-3 heavy chain disease proteins - human  
 C/Species: Homo sapiens (man)  
 C/Date: 31-Dec-1979 #sequence\_revision 23-Oct-1981 #text\_change 16-Jul-1999  
 C/Accession: A90442; A92219; A90198; A93915; A02149  
 R/Frangione, B.; Rosenwasser, E.; Prell, F.; Franklin, E.C.  
 Biochemistry 19, 4304-4308, 1980  
 A/Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-  
 A/Reference number: A90442; PMID:81021548; PMID:6774747  
 A/Contents: heavy chain disease protein wis  
 A/Accession: A90442  
 A/Molecule type: protein  
 A/Residues: 1-289 <FRA>  
 A/Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain  
 A/Note: the sequence of residues 42-76 was taken from the reference that follows  
 J. Michaelson, T.E.; Frangione, B.; Franklin, E.C.  
 J. Biol. Chem. 252, 883-889, 1977

Query Match 84.4%; Score 1169; DB 2; Length 377;  
 Best Local Similarity 92.6%; Pred. No. 2.7e-81;  
 Matches 214; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

A/Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication  
A/Reference number: A92219; PMID:77118561; PMID:403363  
A/Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W  
A/Accession: A92219  
A/Molecule type: protein  
A/Residues: 12-97 <MIC>  
A/Note: the hinge region in gamma-3 chains is about four times as long as in other gamma  
idue segment (12-28)  
A/Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter  
R/Molefstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.  
Biochem. Biophys. Res. Commun. 71, 907-914, 1976  
A/Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the  
A/Reference number: A90194; PMID:77021516; PMID:823945  
A/Contents: heavy chain disease protein ZUC, partial sequence corresponding to residues  
A/Accession: A90198  
A/Molecule type: protein  
A/Residues: 59-125, 'E', 128-226, 228-289 <MOI>  
A/Note: this protein lacks most of the V region, all of the CH1 region, and part of the  
R/Alexander, A.; Steinmetz, M.; Barltault, D.; Frangione, B.; Franklin, E.C.; Hood, L.;  
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982  
A/Title: gamma heavy chain disease in man: CDNA sequence supports partial gene deletion  
A/Reference number: A93915; PMID:62247835; PMID:6808505  
A/Contents: heavy chain disease protein Omm  
A/Accession: A93915  
A/Molecule type: mRNA  
A/Residues: 12-70/72-114/116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-157  
A/Note: a carboxyl-terminal lys is removed posttranslationally  
A/Note: this sequence may represent an allelic form or another gamma chain subclass  
C/Comment: The heavy chain disease protein wis is shown.  
C/Genetics:  
A/Gene: GDB:IGHG3  
A/Cross-references: GDB:119339; OMIM:147120  
A/Map position: 14q32.33-14q32.33  
C/Superfamily: immunoglobulin C region; immunoglobulin homology  
C/Keywords: duplication; glycoprotein; immunoglobulin; pyroglyutamic acid  
F/203-270/Domain: immunoglobulin homology <IMM>  
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F/6.140/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 83.1%; Score 1151; DB 1; Length 289;  
Best Local Similarity 90.5%; Pred. No. 4.5e-80;  
Matches 209; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTCPCPAPBELLGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 59 EPKSCDTPPCPCPCAPBELLGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 118  
QY 61 NWYVDGVEVNAKTKPREEQNSTFRVSVLTVLHODMLNGEKYCKVSNKALPAPIEK 120  
DB 119 KMYVDGVEVNAKTKPREEQNSTFRVSVLTVLHODMLNGEKYCKVSNKALPAPIEK 178  
QY 121 ISKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGYFSPSDIAVEMESNGQPENNYK 180  
DB 179 ISKTKQPREPOVYTLPPSRDELTKNOVSLTCLVKGYFSPSDIAVEMESNGQPENNYK 238  
QY 181 PVLDSGSEFELYKLTVDKSRQOGNWFVSCVHAEALHNHYTQKSLSLSPG 231  
DB 239 PMUDSGSEFELYKLTVDKSRQOGNWFVSCVHAEALHNHYTQKSLSLSPG 289

RESULT 8  
G2HD  
Ig gamma-2 chain C region - human  
C/Species: Homo sapiens (man)  
C/Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #ext\_change 09-Jul-2004  
C/Accession: A93906; A92809; A90752; A93132; A02148  
R/Blissom, J.; Hood, L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982  
A/Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con  
A/Reference number: A93906; PMID:82197621; PMID:6804948  
A/Accession: A93906  
A/Molecule type: DNA  
A/Residues: 1-326 <ELL>

A/Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:932759; PIDN:CAB58438.1; P  
A/Note: Lys-326 is probably removed posttranslationally  
A/Note: A.C.; Tung, E.; Fudenberg, H.H.  
J. Immunol. 125, 1048-1054, 1980  
A/Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and fu  
A/Reference number: A92809; PMID:81007873; PMID:6774012  
A/Contents: myeloma protein T11  
A/Accession: A92809  
A/Molecule type: protein  
A/Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <MAN>  
A/Note: Trp-156 is at or near the complement-binding site  
R/Connell, G.E.; Parr, D.M.; Hofmann, T.  
Can. J. Biochem. 57, 758-767, 1979  
A/Title: The amino acid sequences of the three heavy chain constant region domains of a l  
A/Reference number: A90752; PMID:80001357; PMID:113060  
A/Contents: myeloma protein Z1e  
A/Accession: A90752  
A/Molecule type: protein  
A/Residues: 1-24, 'E', 26-57, 'W', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-;  
A/Note: this sequence has since been revised  
R/Hofmann, T.; Parr, D.M.  
Mol. Immunol. 16, 923-925, 1979  
A/Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin ge  
A/Reference number: A93132; PMID:80114419; PMID:118920  
A/Contents: Z1e  
A/Accession: A93132  
A/Molecule type: protein  
A/Residues: 238-275 <HOF>  
R/Hofmann, T.; Parr, D.M.  
submitted to the Atlas, March 1980  
A/Reference number: A94591  
A/Contents: annotation; Z1e  
A/Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic  
ned  
R/Milestein, C.; Frangione, B.  
Biochem. J. 121, 217-225, 1971  
A/Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.  
A/Reference number: A90251; PMID:72033500; PMID:4940472  
A/Contents: annotation; myeloma protein S8, disulfide bonds  
R/Frangione, B.; Milestein, C.; Plink, J.R.L.  
Nature 221, 145-148, 1969  
A/Title: Structural studies of immunoglobulin G.  
A/Reference number: A93157; PMID:69064124; PMID:5782707  
A/Contents: annotation; S8, disulfide bonds  
C/Genetics:  
A/Gene: GDB:IGHG2  
A/Cross-references: GDB:119338; OMIM:147110  
A/Map position: 14q32.33-14q32.33  
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C/Superfamily: immunoglobulin C region; immunoglobulin homology  
C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F/20-85/Domain: immunoglobulin homology <IM1>  
F/133-202/Domain: immunoglobulin homology <IM2>  
F/239-306/Domain: immunoglobulin homology <IM3>  
F/14/Disulfide bonds: interchain (to light chain) #status experimental  
F/27-83, 140-200, 246-304/Disulfide bonds: #status experimental  
F/102, 103, 106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F/176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 82.3%; Score 1140; DB 1; Length 326;  
Best Local Similarity 91.3%; Pred. No. 3.6e-79;  
Matches 211; Conservative 9; Mismatches 7; Indels 4; Gaps 2;

QY 1 EPKSCDKHTHTCPCPAPBELLGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 99 EPKCCV---CPCPAPB-VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 154  
QY 61 NWYVDGVEVNAKTKPREEQNSTFRVSVLTVLHODMLNGEKYCKVSNKALPAPIEK 120  
DB 155 KMYVDGVEVNAKTKPREEQNSTFRVSVLTVLHODMLNGEKYCKVSNKALPAPIEK 214  
QY 121 ISKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGYFSPSDIAVEMESNGQPENNYK 180

Db 215 ISKTKGQPREPQYTLPPSEBEMTKQVSLTCLVKGFPSPDIIVEMESNGQPENNYKTTTP 274  
QY 181 PVLDSGSGFFLVSKLTVDKSRMOQGNVFCSCVNHGALHNHYTKSLSLSPG 231  
Db 275 PMLDSGSGFFLVSKLTVDKSRMOQGNVFCSCVNHGALHNHYTKSLSLSPG 325

## RESULT 9

G4HU

Ig gamma-4 chain C region - human

C/Species: Homo sapiens (man)

C/Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 09-Jul-2004

C/Accession: A90933; A90249; A02150

R.Bilison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A/Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A/Reference number: A90933; MID:83157104; PMID:6299662

A/Accession: A90933

A/Molecule type: DNA

A/Residues: 1-327 &lt;ELL&gt;

A/Cross-references: UNIPROT:P01861

A/Note: the sequence was determined from the germline gene

R.Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A/Title: Human immunoglobulin subclases. Partial amino acid sequence of the constant

A/Reference number: A90249; MID:70207560; PMID:4192659

A/Accession: A90249

A/Molecule type: protein

A/Residues: 1-30;81-326 &lt;PIN&gt;

C/Genetics:

A/Genes: GDB:IGHG4

A/Cross-references: GDB:119340; OMIM:147130

A/Map position: 14q32.33-14q32.33

A/Introns: 99/1; 111/1; 221/1

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

chain disulfide bonds. In some cases, such as Iga and IgM, the subunits associate into 1a

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F/20-85/Domain: immunoglobulin homology &lt;IML&gt;

F/99-110/Region: hinge

F/134-203/Domain: immunoglobulin homology &lt;IM2&gt;

F/240-307/Domain: immunoglobulin homology &lt;IM3&gt;

F/14/Disulfide bonds: interchain (to light chain) #status experimental

F/27-83,141-201,247-305/Disulfide bonds: #status predicted

F/106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F/177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 81.6%; Score 1130; DB 1; Length 327;

Best Local Similarity 93.7%; Pred. No. 2.1e-78;

Matches 207; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 11 CPBPAPELLGDSVFLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKENYVDGEVH 70

Db 106 CPBPAPELLGDSVFLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKENYVDGEVH 165

QY 71 NAKTKREBOYNTYRVSVLTCLVKGFPSPDIIVEMESNGQPENNYKTTTPVLDSDGSPF 190

Db 166 NAKTKREBOYNTYRVSVLTCLVKGFPSPDIIVEMESNGQPENNYKTTTPVLDSDGSPF 225

QY 131 PLYVTLPPSRDELTKQVSLTCLVKGFPSPDIIVEMESNGQPENNYKTTTPVLDSDGSPF 190

Db 226 PLYVTLPPSRDELTKQVSLTCLVKGFPSPDIIVEMESNGQPENNYKTTTPVLDSDGSPF 285

QY 191 LYSKLTVDKSRMOQGNVFCSCVNHGALHNHYTKSLSLSPG 231

Db 286 LYSKLTVDKSRMOQGNVFCSCVNHGALHNHYTKSLSLSPG 326

RESULT 10

G3MSM

Ig gamma-3 chain C region, membrane-bound form - mouse

C/Species: Mus musculus (house mouse)

C/Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 09-Jul-2004

C/Accession: A90933; A90249; A02150

R.Bilison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A/Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A/Reference number: A90933; MID:83157104; PMID:6299662

A/Accession: A90933

A/Molecule type: DNA

A/Residues: 1-327 &lt;ELL&gt;

A/Cross-references: UNIPROT:P01861

A/Note: the sequence was determined from the germline gene

R.Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A/Title: Human immunoglobulin subclases. Partial amino acid sequence of the constant

A/Reference number: A90249; MID:70207560; PMID:4192659

A/Accession: A90249

A/Molecule type: protein

A/Residues: 1-30;81-326 &lt;PIN&gt;

C/Genetics:

A/Genes: GDB:IGHG4

A/Cross-references: GDB:119340; OMIM:147130

A/Map position: 14q32.33-14q32.33

A/Introns: 99/1; 111/1; 221/1

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

chain disulfide bonds. In some cases, such as Iga and IgM, the subunits associate into 1a

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F/20-85/Domain: immunoglobulin homology &lt;IML&gt;

F/99-110/Region: hinge

F/134-203/Domain: immunoglobulin homology &lt;IM2&gt;

F/240-307/Domain: immunoglobulin homology &lt;IM3&gt;

F/14/Disulfide bonds: interchain (to light chain) #status experimental

F/27-83,141-201,247-305/Disulfide bonds: #status predicted

F/106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F/177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 81.6%; Score 1130; DB 1; Length 327;

Best Local Similarity 93.7%; Pred. No. 2.1e-78;

Matches 207; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 11 CPBPAPELLGDSVFLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKENYVDGEVH 70

Db 106 CPBPAPELLGDSVFLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKENYVDGEVH 165

QY 71 NAKTKREBOYNTYRVSVLTCLVKGFPSPDIIVEMESNGQPENNYKTTTPVLDSDGSPF 190

Db 166 NAKTKREBOYNTYRVSVLTCLVKGFPSPDIIVEMESNGQPENNYKTTTPVLDSDGSPF 225

QY 131 PLYVTLPPSRDELTKQVSLTCLVKGFPSPDIIVEMESNGQPENNYKTTTPVLDSDGSPF 190

Db 226 PLYVTLPPSRDELTKQVSLTCLVKGFPSPDIIVEMESNGQPENNYKTTTPVLDSDGSPF 285

QY 191 LYSKLTVDKSRMOQGNVFCSCVNHGALHNHYTKSLSLSPG 231

Db 286 LYSKLTVDKSRMOQGNVFCSCVNHGALHNHYTKSLSLSPG 326

RESULT 11

G1MSM

Ig gamma-1 chain C region, membrane-bound form - mouse

C/Species: Mus musculus (house mouse)

C/Date: 17-Dec-1982 #sequence\_revision 31-Mar-1991 #text\_change 09-Jul-2004

C/Accession: B02159; A02160; B02158

R.Honjo, T.; Obara, M.; Yamawaki-Kataoka, Y.; Kataoka, T.; Kawakami, T.; Takahashi, N.;

Cell 18, 559-568, 1979

A/Title: Cloning and complete nucleotide sequence of mouse immunoglobulin gamma1 chain

A/Reference number: A02159; MID:80045036; PMID:115553

A/Accession: B02159

A/Molecule type: DNA

A/Residues: 1-393 &lt;HON&gt;

A/Cross-references: UNIPROT:P01869; GB:J00453

C/Date: 13-Aug-1986 #sequence\_revision 31-Mar-1991 #text\_change 09-Jul-2004  
C/Accession: A02156; A02155  
R.Honjo, T.A.; Word, C.J.; Rimm, D.; Der-Balan, G.P.; Martinez, H.M.; Tucker, P.W.; Blactr  
EMBO J. 3, 12041-2046, 1984  
A/Title: Structure analysis of the murine IgG3 constant region gene.  
A/Reference number: A02156; MID:85027161; PMID:6092053  
A/Accession: A02156

## RESULT 11

G1MSM

Ig gamma-1 chain C region, membrane-bound form - mouse

C/Species: Mus musculus (house mouse)

C/Date: 17-Dec-1982 #sequence\_revision 31-Mar-1991 #text\_change 09-Jul-2004

C/Accession: B02159; A02160; B02158

R.Honjo, T.; Obara, M.; Yamawaki-Kataoka, Y.; Kataoka, T.; Kawakami, T.; Takahashi, N.;

Cell 18, 559-568, 1979

A/Title: Cloning and complete nucleotide sequence of mouse immunoglobulin gamma1 chain

A/Reference number: A02159; MID:80045036; PMID:115553

A/Accession: B02159

A/Molecule type: DNA

A/Residues: 1-393 &lt;HON&gt;

A/Cross-references: UNIPROT:P03967; GB:J00451; MID:9194392; PIDN:AA59655.1; PID:9194433

A/Note: the sequence was determined from the germline gene

R.Komatsu, M.; Clayton, L.; Rogers, J.; Robertson, S.; Kettman, J.; Wall, R.

Nucleic Acids Res. 11, 6775-6785, 1983

A/Title: The structure of the mouse immunoglobulin in gamma-3 membrane gene segment.

A/Reference number: A02155; MID:84041483; PMID:6314258

A/Accession: A02155

A/Molecule type: DNA

A/Residues: 328-332, 'G', 334-341, 'Q', 343-387, 'F', 389-398 &lt;KOM&gt;

A/Cross-references: GB:K00688

A/Note: the sequence was determined from the germline gene

C/Genetics:

A/Introns: 97/1, 113/1, 223/1, 328/1; 371/3

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

chain disulfide bonds. In some cases, such as Iga and IgM, the subunits associate into 1a

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin

F/19-83/Domain: immunoglobulin homology &lt;IM1&gt;

F/97-112/Region: hinge

F/136-205/Domain: immunoglobulin homology &lt;IM2&gt;

F/242-309/Domain: immunoglobulin homology &lt;IM3&gt;

F/346-362/Domain: transmembrane #status predicted &lt;TM&gt;

F/363-398/Domain: intracellular #status predicted &lt;INT&gt;

F/179,322/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.8%; Score 938.5; DB 1; Length 398;

Best Local Similarity 68.4%; Pred. No. 9e-64;

Matches 167; Conservative 36; Mismatches 38; Indels 3; Gaps 1;

QY 12 PR---CPBPELLGDSVFLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKENYVDGEVH 68

Db 106 PRSSCPBNITLGGPSVFLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKENYVDGEVH 165

QY 69 VNAKTKREBOYNTYRVSVLTCLVKGFPSPDIIVEMESNGQPENNYKTTTPVLDSDGSPF 128

Db 166 VNAKTKREBOYNTYRVSVLTCLVKGFPSPDIIVEMESNGQPENNYKTTTPVLDSDGSPF 225

QY 129 REPQVYTLPPSRDELTKQVSLTCLVKGFPSPDIIVEMESNGQPENNYKTTTPVLDSDGSPF 188

Db 226 REPQVYTLPPSRDELTKQVSLTCLVKGFPSPDIIVEMESNGQPENNYKTTTPVLDSDGSPF 285

QY 189 FPLYSKLTVDKSRMOQGNVFCSCVNHGALHNHYTKSLSLSPG 248

Db 286 FPLYSKLTVDKSRMOQGNVFCSCVNHGALHNHYTKSLSLSPG 345

QY 249 LMTT 252

Db 346 LMTT 349

RESULT 11

G1MSM

Ig gamma-1 chain C region, membrane-bound form - mouse

C/Species: Mus musculus (house mouse)

C/Date: 17-Dec-1982 #sequence\_revision 31-Mar-1991 #text\_change 09-Jul-2004

C/Accession: B02159; A02160; B02158

R.Honjo, T.; Obara, M.; Yamawaki-Kataoka, Y.; Kataoka, T.; Kawakami, T.; Takahashi, N.;

Cell 18, 559-568, 1979

A/Title: Cloning and complete nucleotide sequence of mouse immunoglobulin gamma1 chain

A/Reference number: A02159; MID:80045036; PMID:115553

A/Accession: B02159

A/Molecule type: DNA

A/Residues: 1-393 &lt;HON&gt;

A/Cross-references: UNIPROT:P01869; GB:J00453

A>Note: the sequence was determined from the germ-line gene  
 R.Tyler, B.M.; Cowman, A.F.; Gerondakis, S.D.; Adams, J.M.; Bernard, O.  
 Proc. Natl. Acad. Sci. U.S.A. 79, 2008-2012, 1982  
 A>Title: mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane  
 A:Reference number: A02160; MUID:82197626; PMID:6804950  
 A:Accession: A02160  
 A:Molecule type: mRNA  
 A:Residues: 323-393 <TYL>  
 R.Rogers, J., Choi, E.; Souza, L.; Carter, C.; Word, C.; Kuehl, M.; Eisenberg, D.; Wall, R.  
 Cell 26, 19-27, 1981  
 A>Title: Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma C  
 A:Reference number: A02158; MUID:82115295; PMID:6799207  
 A:Accession: B02158  
 A:Molecule type: DNA  
 A:Residues: 323-366 <ROG>  
 A>Note: this sequence is the translation of the first exon of the M segment  
 C:Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The m  
 ncode membrane-bound chains in that it contains an alternative 3' end, encoded in separa  
 C:Genetics:  
 A:Insertions: 1/1; 98/1; 111/1; 218/1; 323/1; 366/3  
 C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kap  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: alternative splicing; duplication; glycoprotein; heterotrimer; immunoglobu  
 C:131-200/Domain: immunoglobulin homology <IM>  
 F:131-200/Domain: immunoglobulin homology <IM>  
 F:340-357/Domain: transmembrane #status predicted <INT>  
 F:358-393/Domain: intracellular #status predicted <INT>  
 F:174-278/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.3%; Score 931.5; DB 1; Length 393;  
 Best Local Similarity 64.0%; Pred. No. 3e-63; Indels 9; Gaps 3;  
 Matches 162; Conservative 45; Mismatches 37;

2 PKSCDKHTHCP--CPAPPELLGSPSVFLFPKPKDTMTLSRTEVTVVDSHEDPEVK 59  
 Db 99 PRDGG---KPCCTCTYPEV---SSVIFPPKPKDVLTLTPKVCVVVDISKDPEVQ 151  
 Oy 60 FNNVYDGEVHNATKPRREOYNSTYRVSVLTVLHODMNGKRYKKVKNKLLPAPTEK 119  
 Db 152 FSWFVDVGEVHTAQTPREOQFNSTFRSVSELPTMHDWNGKPKCKRVNSAAPPATIEK 211  
 Oy 120 TTSRAKQPRPPOVYTLPPSRDELTKNQVSLTCLVKGPSPSDIAVEMESNQPPENNYKT 179  
 Db 212 TTSKKGPRKAPQVYTLTPPEKQMAKDKVSLTCTMTDPFEDIVEMQNGPAPENNYKT 271  
 Oy 180 PVLVDSGSPFLYSKLTVDKSRMOQGNVSCSVNHEALHNHYTKSLSLSGLOLDEPCA 239  
 Db 272 QPIMNTNGSYFYSLTANQKSNWEGNFTCSVLHGLHNHTEKSLSHSPGLDLETCA 331

Oy 240 EAQDGEGLDGLMTT 252  
 Db 332 EAQDGEGLDGLMTT 344

RESULT 12  
 GHRB  
 Ig gamma chain C region - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 24-Apr-1984 #sequence\_revision 15-Nov-1984 #text\_change 09-Jul-2004  
 C:Accession: A91749; A90290; A93928; A90245; A94416; A02161  
 R.Bernstein, K.E.; Alexander, C.B.; Mage, R.G.  
 Immunogenetics 19, 387-397, 1983  
 A>Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-1 haplot  
 A:Reference number: A91749; MUID:84030950; PMID:6133520  
 A:Accession: A91749  
 A:Molecule type: mRNA  
 A:Residues: 1-323 <BER>  
 A:Cross-references: UNIPROT:P01870  
 A>Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr  
 R.Pratt, D.M.; Mole, L.B.  
 Biochem. J. 151, 337-349, 1975  
 A>Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglob  
 A:Reference number: A90290; MUID:76135469; PMID:1243651

A:Accession: A90290  
 A:Molecule type: protein  
 A:Residues: 1-47, 'E', 49-71, 'EV', 72-128 <PRA>  
 R.Martens, C.L.; Moore, K.W.; Steimetz, M.; Hood, L.; Knight, K.L.  
 Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982  
 A>Title: Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma heavy chain  
 A:Reference number: A93928; MUID:83299917; PMID:6193512  
 A:Accession: A93928  
 A:Molecule type: mRNA  
 A:Residues: 88-103, 'W', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>  
 A:Cross-references: GB:M16426; NID:9165111; PIRN:AAA1289.1; PID:9165112  
 A>Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker  
 R.Fruehr, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.  
 Biochem. J. 116, 249-259, 1970  
 A>Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin C  
 A:Reference number: A90245; MUID:70110015; PMID:5461106  
 A:Accession: A90245  
 A:Molecule type: protein  
 A:Residues: 132-143, 'E', 145-161 <FRU>  
 R.Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.  
 In Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell,  
 A:Reference number: A94416  
 A:Accession: A94416  
 A:Molecule type: protein  
 A:Residues: 129-131, 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'Q', 'Z'  
 A>Note: this has the e15 allotypic marker, 185-Ala  
 C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kap  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin  
 F:20-82/Domain: immunoglobulin homology <IM1>  
 F:130-199/Domain: immunoglobulin homology <IM2>  
 F:236-303/Domain: immunoglobulin homology <IM3>  
 F:173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 66.1%; Score 916; DB 1; Length 323;  
 Best Local Similarity 67.2%; Pred. No. 3.5e-62;  
 Matches 166; Conservative 31; Mismatches 34; Indels 16; Gaps 2;

1 EPKSCDKTH-----TC--PPCAPPELLGSPSVFLFPKPKDTMTLSRTEV 44  
 Db 76 QPVTGNVAHPATNTKVDKTVAPSTCSKPTCPPELLGSPSVIFPPKPKDTMTLSRTEV 135  
 Oy 45 TCYVVDVSHEDPEVKKNWVVDGEVHNATKPRREOYNSTYRVSVLTVLHODMNGKEY 104  
 Db 136 TCYVVDVSDDDPEVQFTWYINNEVHTAPPRPRBEQFNSTIRVSLTPTHQDWKGEF 195  
 Oy 105 KCKVSNKALPAPTEKTSRAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGPSPSDIAV 164  
 Db 196 KCKVHNKALPAPTEKTSRAKQPREPOVYTLWGPSPREELSSRSVSLTCMINGPYSDISV 255  
 Oy 165 EWSNQPPENNYKTTPPVLDSDGSFPLYSKLTVDKSRMOQGNVSCSVNHEALHNHYTK 224  
 Db 256 EWEKNGKAEEDNYKTPAVLDSDGSFPLYNKLSVTSBWKQGDVFTCSVNHEALHNHYTK 315

Oy 225 SLSTSPG 231  
 Db 316 SLSTSPG 322

RESULT 13  
 GMSM  
 Ig gamma-2a chain C region, membrane-bound form - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 19-Feb-1984 #sequence\_revision 31-Mar-1991 #text\_change 09-Jul-2004  
 C:Accession: A02154; B32657; I57809  
 R.Yamawaki-Kataoka, Y.; Nakai, S.; Miyata, T.; Honjo, T.  
 Proc. Natl. Acad. Sci. U.S.A. 79, 2623-2627, 1982  
 A>Title: Nucleotide sequences of gene segments encoding membrane domains of immunoglobul  
 A:Reference number: A02154; MUID:8222190; PMID:6283537  
 A:Accession: A02154  
 A:Molecule type: DNA  
 A:Residues: 329-399 <YAM>

A/Cross-references: UNIPROT:P01865; GB:J00471  
 A/Note: the sequence was determined from the germ-line gene  
 R:Yamawaki-Karaoaka, Y.; Miyata, T.; Honjo, T.  
 Nucleic Acids Res. 9, 1365-1381, 1981  
 A/Title: The complete nucleotide sequence of mouse immunoglobulin gamma 2 A gene and env  
 A/Reference number: A32657; MUID:8118976; PMID:6262729  
 A/Accession: B32657  
 A/Molecule type: DNA  
 A/Residues: 1-329; 'K' <Y>  
 R:Hall, B.; Milcarek, C.  
 Mol. Immunol. 26, 819-826, 1989  
 A/Title: Sequence and polyadenylation site determination of the murine immunoglobulin gamma 2A gene  
 A/Reference number: 157809; MUID:90097953; PMID:2513486  
 A/Accession: 157809  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 373-399 <RES>  
 A/Cross-references: GB:M35032; NID:9194478; PIDN:AAA37919.1; PID:9387217  
 C/Species: The sequence of residues 1-328 was assumed to be identical with the corresponding C/Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The major one has a 3' end, encoded in separate exons, that is homologous with C/Genetics: 1/1; 98/1; 114/1; 224/1; 329/1; 372/1  
 A/Functions: 1/1; 98/1; 114/1; 224/1; 329/1; 372/1  
 C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger C/Superfamily: immunoglobulin C region; immunoglobulin homology  
 C/Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin F/137-206/Domain: immunoglobulin homology <IMM>  
 F/346-363/Domain: transmembrane #status predicted <TM>  
 F/364-399/Domain: intracellular #status predicted <INT>  
 F/180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 65.3%; Score 905; DB 1; Length 399;  
 Best Local Similarity 66.8%; Pred. No. 3.1e-61;

Matches 163; Conservative 31; Mismatches 48; Indels 2; Gaps 1;

QY 11 CPPEBELLGGPSVFLPPPKKDTLMISRTPEVTCVVDVSHDEPEKFMVYDGEV 68  
 DB 107 CPCKCPANLGGPSVFLPPPKKDTLMISRTPEVTCVVDVSHDEPEKFMVYDGEV 166  
 QY 69 VNAKTPREBOYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGP 128  
 DB 167 VTAQOTREDFNSTLRVVSALPIQHODWMSGKEPKCKVNNKDLPAPIEKTISKAKGP 226  
 QY 129 RRPQVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGS 188  
 DB 227 RRPQVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGS 286  
 QY 189 PFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGQLDETCAADGELDG 248  
 DB 287 YFMYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGQLDETCAADGELDG 346  
 QY 249 LMTT 252  
 DB 347 LMTT 350

RESULT 14

147160  
 Ig gamma 2b chain constant region - pig (fragment)  
 C/Species: Sus scrofa domestica (domestic pig)  
 C/Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
 C/Accession: 147160  
 R:Kacskovics, I.; Sun, J.; Butler, J.E.  
 J. Immunol. 153, 3565-3573, 1994  
 A/Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
 A/Reference number: 147158; MUID:95015845; PMID:7930579  
 A/Accession: 147160  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-328 <KAC>  
 A/Cross-references: EMBL:U03760; NID:9433125; PIDN:AAA52218.1; PID:9433126  
 C/Genetics:

A/Genes: IgG2b  
 C/Superfamily: immunoglobulin C region; immunoglobulin homology  
 F/133-202/Domain: immunoglobulin homology <IMM>

Query Match 65.1%; Score 901.5; DB 2; Length 328;  
 Best Local Similarity 73.1%; Pred. No. 4.5e-61;  
 Matches 163; Conservative 29; Mismatches 28; Indels 3; Gaps 2;

QY 11 CPPEBELLGGPSVFLPPPKKDTLMISRTPEVTCVVDVSHDEPEKFMVYDGEV 70  
 DB 106 CPICPACB-SPGSVFIPPPKPDITMISRTPEVTCVVDVSHDEPEKFMVYDGEV 164  
 QY 71 NAKTPREBOYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGP 130  
 DB 165 TAQTRKEQFNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGP 224  
 QY 131 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGS 188  
 DB 225 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGS 284  
 QY 189 PFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 231  
 DB 285 YFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 327

RESULT 15

147159  
 Ig gamma 2a chain constant region - pig (fragment)

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000

C/Accession: 147159

R:Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A/Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a

A/Reference number: 147158; MUID:95015845; PMID:7930579

A/Accession: 147159

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-328 <KAC>

A/Cross-references: EMBL:U03779; NID:9433123; PIDN:AAA52217.1; PID:9433124

C/Genetics:

A/Genes: IgG2a

C/Superfamily: immunoglobulin C region; immunoglobulin homology

F/133-202/Domain: immunoglobulin homology <IMM>

Query Match 65.1%; Score 901.5; DB 2; Length 328;  
 Best Local Similarity 73.1%; Pred. No. 4.5e-61;

Matches 163; Conservative 29; Mismatches 28; Indels 3; Gaps 2;

QY 11 CPPEBELLGGPSVFLPPPKKDTLMISRTPEVTCVVDVSHDEPEKFMVYDGEV 70  
 DB 106 CPICPACB-SPGSVFIPPPKPDITMISRTPEVTCVVDVSHDEPEKFMVYDGEV 164  
 QY 71 NAKTPREBOYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGP 130  
 DB 165 TAQTRKEQFNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGP 224  
 QY 131 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGS 188  
 DB 225 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGS 284  
 QY 189 PFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 231  
 DB 285 YFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 327

Search completed: March 7, 2005, 07:20:59  
 Job time : 20.6798 secs

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